REMARKS

Claims 10-15 are pending in the application. Claims 10, 13 and 14 have been amended to better clarify what Applicants regard as the invention. No new matter has been added by way of this amendment. Thus, as a result of the foregoing amendment, claims 10 through 15 remain under consideration. Reconsideration of this application is respectfully requested.

The amended claims are shown above without markings. Attached hereto is a version with markings to show the changes made, captioned "Version with markings to show changes made."

Claims 10-15 are rejected under 35 U.S.C. §112, second paragraph for being indefinite. Applicants respectfully traverse the Examiner's rejection, and have also amended the claims to better clarify what Applicants regard as the invention. Support for the amendments can be found on page 5, lines 1-6 and 27-29, on page 7, lines 12-30 and on page 18, lines 15-29. Thus, withdrawal of the rejection under 35 U.S.C. §112, second paragraph, is respectfully requested.

Claims 10-15 have been rejected under 35 U.S.C. §112, first paragraph for not fulfilling the written description requirement. Applicants respectfully traverse the Examiner's rejection and have also amended the claims to better clarify the invention. Support for the amendments can be found on page 5, lines 27-29, and on page 7, lines 12-30. Thus, Applicants respectfully request withdrawal of the rejection under 35 U.S.C. §112, first paragraph.

***Claim Rejections under 35 U.S.C. §112***

The Examiner has rejected claims 10-15 under 35 U.S.C. 112, second paragraph for being vague and indefinite. Applicants respectfully traverse Examiner's rejection and have amended the claims to better clarify what Applicants regard as the invention. Furthermore, Applicants refer the Examiner to the specification on page 18, lines 15-29, whereby the "standard hybridization conditions" are defined as being equivalent to 5x SSC and 65°C for both hybridization and wash. In addition, Applicants have amended the claims to point out the specific functionality associated with the degenerate variants that bind under standard

hybridization conditions. In particular, the term "degenerate variants" as known to one skilled in the art is used to reflect the fact that due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as TRIP may be used in the practice of the present invention including those comprising conservative substitutions thereof. These include but are not limited to degenerate variants which are altered by the substitution of different codons that encode the same amino acid residue within the sequence, thus producing a silent change. By way of example, the term "degenerative variants" has a meaning that is well known in the extant art; and the Examiner is referred to U.S. Patent No. 6,569,662 at column 20, lines 15 through 22 for a discussion of this term. A copy of this patent is enclosed for the Examiner's convenience.

The Examiner has further rejected claims 10-15 under 35 U.S.C. §112, first paragraph for not complying with the written description requirement. Applicants respectfully traverse the rejection, and have amended the claims to read on the human and mouse sequences identified as SEQ ID NOs: 7 and 8, having specific functionality associated with the TRIP protein encoded by the two sequences.

The Examiner further asserts that the metes and bounds for the terms "degenerate variant" and "hybridize" are not clear. Furthermore, the Examiner asserts that it is unclear as to what the limits of the structure and function are. Applicants respectfully traverse Examiner's rejections for the following reasons. Applicants refer the Examiner to page 40, lines 16 through 23, wherein it is noted that:

> "The yeast two-hybrid assay was used to determine the structural requirements for the interaction of TRIP with TRAF1 or TRAF2. In the yeast two-hybrid assay, a mutant TRIP comprising the N-terminal half of the protein (residues 1-275 in FIGURE 2A) interacted with TRAFs whereas a mutant TRIP lacking the N-terminal RING finger and the coiled-coil domain (residues 275-470 in FIGURE 2A) failed to interact with the TRAFs."

Furthermore, page 44, lines 1 through 3, indicate that the putative coiled-coil domain of TRIP is required to inhibit TRAF2 mediated NF-kB activation. In addition, on page 44, lines 18-26, Applicants note:

> "The inhibition of NF-kB activation by TRIP required the same domains of TRIP which mediates the interaction. An N- terminal deletion mutant of TRIP which lacks the TRIP-TRAF interaction domain (residues 275-470 in FIGURE 2A) failed to inhibit TRAF2- mediated NF-kB activation. Moreover, a C- terminal deletion mutant of TRIP containing the N-terminal RING finger motif and the putative coiled-coil domain (residues 1-185 in FIGURE 2A) was sufficient to inhibit TRAF2-mediated NF-kB activation."

Applicants respectfully point out that the structural requirements for functional activity, ie. the sequences encoding the functional protein domains as demonstrated in the specification as shown above, are encompassed in the total nucleic acid sequences provided in SEQ ID NOs: 7 and 8, as claimed. Thus, the regions which are critical to the structure and function of the genus claimed have been outlined as described above. Furthermore, the functional limitation of the "degenerate variants" which hybridize to the human and mouse sequences under standard hybridization conditions, as provided herein, is more clearly defined in the claims as amended.

In light of the foregoing arguments and in light of the claim amendments, withdrawal of the rejection is respectfully requested.

***Fees***

No fees are believed to be necessitated by the instant response. However, should this be in error, authorization is hereby given to charge Deposit Account No. 11-1153 for any underpayment, or to credit any overpayments.

***Conclusion***

Applicants believe that the foregoing amendments to the claims place the application in condition for allowance. Withdrawal of the rejections and objections is respectfully requested. If a discussion with the undersigned will be of assistance in resolving any remaining issues, the Examiner is invited to telephone the undersigned at (201) 487-5800, ext. 118, to effect a resolution.

Respectfully submitted,

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Enclosures: Version with Markings to Show Changes Made;
US Patent No: 6,569,662

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

IN THE CLAIMS:

The following amended claims 10, 13 and 14 are to replace the pending claims having the same claim numbers:

10. (Amended) A DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, selected from the group consisting of the nucleotide sequences shown in FIGURE 8 (SEQ ID NO: 7) (SEQ ID NO: 8), DNA sequences that hybridize to any of the foregoing DNA sequences under standard hybridization conditions and DNA sequences that code on expression for an amino acid sequence encoded by any of the foregoing DNA sequences, wherein said DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, regulates TRAF-2 mediated NF-kB activation.

13. (Amended) A recombinant DNA molecule comprising a DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, selected from the group consisting of the nucleotide sequences shown in FIGURE 8 (SEQ ID NO: 7) (SEQ ID NO: 8), DNA sequences that hybridize to any of the foregoing DNA sequences under standard hybridization conditions and DNA sequences that code on expression for an amino acid sequence encoded by any of the foregoing DNA sequences, wherein said DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, regulates TRAF-2 mediated NF-kB activation.

14. (Amended) A unicellular host transformed with a recombinant DNA molecule comprising a DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, selected from the group consisting of the nucleotide sequences shown in FIGURE 8 (SEQ ID NO: 7) (SEQ ID NO: 8), DNA sequences that hybridize to any of the foregoing DNA sequences under standard hybridization conditions and DNA sequences that code on expression for an amino acid sequence encoded by any of the foregoing DNA sequences, wherein said DNA sequence or degenerate variant thereof, which encodes TRIP or a fragment thereof, regulates TRAF-2 mediated NF-kB activation.